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## RAW SEQUENCE LISTING

DATE: 09/17/2004

PATENT APPLICATION: US/10/788,992

TIME: 08:55:02

Input Set : N:\Crif3\RULE60\10788992.raw.txt

Output Set: N:\CRF4\09172004\J788992.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Gilula, Norton B

6 Cravatt, Benjamin F

7 Lerner, Richard A

9 (ii) TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE

11 (iii) NUMBER OF SEQUENCES: 54

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: The Scripps Research Institute

15 (B) STREET: 10550 North Torrey Pines Road

16 (C) CITY: La Jolla

17 (D) STATE: California

18 (E) COUNTRY: US

19 (F) ZIP: 92037

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/788,992

C--> 29 (B) FILING DATE: 26-Feb-2004

30 (C) CLASSIFICATION: 435

32 (vii) PRIOR APPLICATION DATA:

W--> 33 (A) APPLICATION NUMBER: US/08/743,168

34 (B) FILING DATE: 01-May-1998

W--> 35 (A) APPLICATION NUMBER: US 08/489,535

36 (B) FILING DATE: 12-JUN-1995

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Fitting, Thomas

40 (B) REGISTRATION NUMBER: 34,163

41 (C) REFERENCE/DOCKET NUMBER: TSRI 485.2

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (619) 784-2937

45 (B) TELEFAX: (619) 784-9399

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 783 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: double

54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

58 (iii) HYPOTHETICAL: NO

ENTERED

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60      (iv) ANTI-SENSE: NO
63      (ix) FEATURE:
64          (A) NAME/KEY: CDS
65          (B) LOCATION: 1..783
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 AGC CCA GGA GGT TCC TCA GGG GGT GAG GGG GCT CTC ATT GGA TCT GGA      48
71 Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser Gly
72 1      5      10      15
74 GGT TCC CCT CTG GGT TTA GGC ACT GAC ATT GGC GGC AGC ATC CGG TTC      96
75 Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe
76      20      25      30
78 CCT TCT GCC TTC TGC GGC ATC TGT GGC CTC AAG CCT ACT GGC AAC CGC      144
79 Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr Gly Asn Arg
80      35      40      45
82 CTC AGC AAG AGT GGC CTG AAG GGC TGT GTC TAT GGA CAG ACG GCA GTG      192
83 Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val
84      50      55      60
86 CAG CTT TCT CTT GGC CCC ATG GCC CGG GAT GTG GAG AGC CTG GCG CTA      240
87 Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu Ser Leu Ala Leu
88 65      70      75      80
90 TGC CTG AAA GCT CTA CTG TGT GAG CAC TTG TTC ACC TTG GAC CCT ACC      288
91 Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr Leu Asp Pro Thr
92      85      90      95
94 GTG CCT CCC TTT CCC TTC AGA GAG GAG GTC TAT AGA AGT TCT AGA CCC      336
95 Val Pro Pro Phe Pro Phe Arg Glu Glu Val Tyr Arg Ser Ser Arg Pro
96      100      105      110
98 CTG CGT GTG GGG TAC TAT GAG ACT GAC AAC TAT ACC ATG CCC AGC CCA      384
99 Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr Met Pro Ser Pro
100      115      120      125
102 GCT ATG AGG AGG GCT CTG ATA GAG ACC AAG CAG AGA CTT GAG GCT GCT      432
103 Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg Leu Glu Ala Ala
104      130      135      140
106 GGC CAC ACG CTG ATT CCC TTC TTA CCC AAC AAC ATA CCC TAC GCC CTG      480
107 Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile Pro Tyr Ala Leu
108 145      150      155      160
110 GAG GTC CTG TCT GCG GGC GGC CTG TTC AGT GAC GGT GGC CGC AGT TTT      528
111 Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly Gly Arg Ser Phe
112      165      170      175
114 CTC CAA AAC TTC AAA GGT GAC TTT GTG GAT CCC TGC TTG GGA GAC CTG      576
115 Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys Leu Gly Asp Leu
116      180      185      190
118 ATC TTA ATT CTG AGG CTG CCC AGC TGG TTT AAA AGA CTG CTG AGC CTC      624
119 Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg Leu Leu Ser Leu
120      195      200      205
122 CTG CTG AAG CCT CTG TTT CCT CGG CTG GCA GCC TTT CTC AAC AGT ATG      672
123 Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe Leu Asn Ser Met
124      210      215      220
126 CGT CCT CGG TCA GCT GAA AAG CTG TGG AAA CTG CAG CAT GAG ATT GAG      720
127 Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln His Glu Ile Glu

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```

128 225          230          235          240
130 ATG TAT CGC CAG TCT GTG ATT GCC CAG TGG AAA GCG ATG AAC TTG GAT      768
131 Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala Met Asn Leu Asp
132          245          250          255
134 GTG CTG CTG ACC TAA
135 Val Leu Leu Thr      783
136          260
139 (2) INFORMATION FOR SEQ ID NO: 2:
141 (i) SEQUENCE CHARACTERISTICS:
142 (A) LENGTH: 260 amino acids
143 (B) TYPE: amino acid
144 (D) TOPOLOGY: linear
146 (ii) MOLECULE TYPE: protein
148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
150 Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser Gly
151 1 5 10 15
153 Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe
154 20 25 30
156 Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr Gly Asn Arg
157 35 40 45
159 Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val
160 50 55 60
162 Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu Ser Leu Ala Leu
163 65 70 75 80
165 Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr Leu Asp Pro Thr
166 85 90 95
168 Val Pro Pro Phe Pro Phe Arg Glu Glu Val Tyr Arg Ser Ser Arg Pro
169 100 105 110
171 Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr Met Pro Ser Pro
172 115 120 125
174 Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg Leu Glu Ala Ala
175 130 135 140
177 Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile Pro Tyr Ala Leu
178 145 150 155 160
180 Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly Gly Arg Ser Phe
181 165 170 175
183 Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys Leu Gly Asp Leu
184 180 185 190
186 Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg Leu Leu Ser Leu
187 195 200 205
189 Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe Leu Asn Ser Met
190 210 215 220
192 Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln His Glu Ile Glu
193 225 230 235 240
195 Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala Met Asn Leu Asp
196 245 250 255
198 Val Leu Leu Thr
199 260
202 (2) INFORMATION FOR SEQ ID NO: 3:

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Output Set: N:\CRF4\09172004\J788992.raw

```

204      (i) SEQUENCE CHARACTERISTICS:
205          (A) LENGTH: 22 base pairs
206          (B) TYPE: nucleic acid
207          (C) STRANDEDNESS: single
208          (D) TOPOLOGY: linear
210      (ii) MOLECULE TYPE: cDNA
212      (iii) HYPOTHETICAL: NO
214      (iv) ANTI-SENSE: NO
218      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
220 CGGAATTCGG NGGNGARGGN GC
222 (2) INFORMATION FOR SEQ ID NO: 4:
224      (i) SEQUENCE CHARACTERISTICS:
225          (A) LENGTH: 5 amino acids
226          (B) TYPE: amino acid
227          (D) TOPOLOGY: linear
229      (ii) MOLECULE TYPE: peptide
231      (v) FRAGMENT TYPE: internal
235      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
237      Gly Gly Glu Gly Ala
238          1          5
240 (2) INFORMATION FOR SEQ ID NO: 5:
242      (i) SEQUENCE CHARACTERISTICS:
243          (A) LENGTH: 31 amino acids
244          (B) TYPE: amino acid
245          (D) TOPOLOGY: linear
247      (ii) MOLECULE TYPE: peptide
249      (v) FRAGMENT TYPE: internal
253      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
255      Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser Gly Gly Ser
256          1          5          10          15
258      Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe Pro
259          20          25          30
261 (2) INFORMATION FOR SEQ ID NO: 6:
263      (i) SEQUENCE CHARACTERISTICS:
264          (A) LENGTH: 15 amino acids
265          (B) TYPE: amino acid
266          (D) TOPOLOGY: linear
268      (ii) MOLECULE TYPE: peptide
270      (v) FRAGMENT TYPE: internal
274      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
276      Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser
277          1          5          10          15
279 (2) INFORMATION FOR SEQ ID NO: 7:
281      (i) SEQUENCE CHARACTERISTICS:
282          (A) LENGTH: 15 amino acids
283          (B) TYPE: amino acid
284          (D) TOPOLOGY: linear
286      (ii) MOLECULE TYPE: peptide
288      (v) FRAGMENT TYPE: internal

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Input Set : N:\Crf3\RULE60\10788992.raw.txt

Output Set: N:\CRF4\09172004\J788992.raw

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292      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
294      Ala Leu Ile Gly Ser Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp
295      1             5             10             15
297 (2) INFORMATION FOR SEQ ID NO: 8:
299      (i) SEQUENCE CHARACTERISTICS:
300          (A) LENGTH: 15 amino acids
301          (B) TYPE: amino acid
302          (D) TOPOLOGY: linear
304      (ii) MOLECULE TYPE: peptide
306      (v) FRAGMENT TYPE: internal
310      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
312      Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe Pro Ser Ala
313      1             5             10             15
315 (2) INFORMATION FOR SEQ ID NO: 9:
317      (i) SEQUENCE CHARACTERISTICS:
318          (A) LENGTH: 15 amino acids
319          (B) TYPE: amino acid
320          (D) TOPOLOGY: linear
322      (ii) MOLECULE TYPE: peptide
324      (v) FRAGMENT TYPE: internal
328      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
330      Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr
331      1             5             10             15
333 (2) INFORMATION FOR SEQ ID NO: 10:
335      (i) SEQUENCE CHARACTERISTICS:
336          (A) LENGTH: 15 amino acids
337          (B) TYPE: amino acid
338          (D) TOPOLOGY: linear
340      (ii) MOLECULE TYPE: peptide
342      (v) FRAGMENT TYPE: internal
346      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
348      Gly Leu Lys Pro Thr Gly Asn Arg Leu Ser Lys Ser Gly Leu Lys
349      1             5             10             15
351 (2) INFORMATION FOR SEQ ID NO: 11:
353      (i) SEQUENCE CHARACTERISTICS:
354          (A) LENGTH: 15 amino acids
355          (B) TYPE: amino acid
356          (D) TOPOLOGY: linear
358      (ii) MOLECULE TYPE: peptide
360      (v) FRAGMENT TYPE: internal
364      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
366      Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val Gln
367      1             5             10             15
369 (2) INFORMATION FOR SEQ ID NO: 12:
371      (i) SEQUENCE CHARACTERISTICS:
372          (A) LENGTH: 15 amino acids
373          (B) TYPE: amino acid
374          (D) TOPOLOGY: linear
376      (ii) MOLECULE TYPE: peptide

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 09/17/2004  
PATENT APPLICATION: US/10/788,992      TIME: 08:55:03

Input Set : N:\Crf3\RULE60\10788992.raw.txt  
Output Set: N:\CRF4\09172004\J788992.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 11,14,20

Seq#:33; N Pos. 14

Seq#:38; Xaa Pos.5

Seq#:54; N Pos. 780,786,789,792,795,798,804,810,813,816,819

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/788,992

DATE: 09/17/2004

TIME: 08:55:03

Input Set : N:\Crf3\RULE60\10788992.raw.txt

Output Set: N:\CRF4\09172004\J788992.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:957 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:35  
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0